



# Blast 2 Sequences results

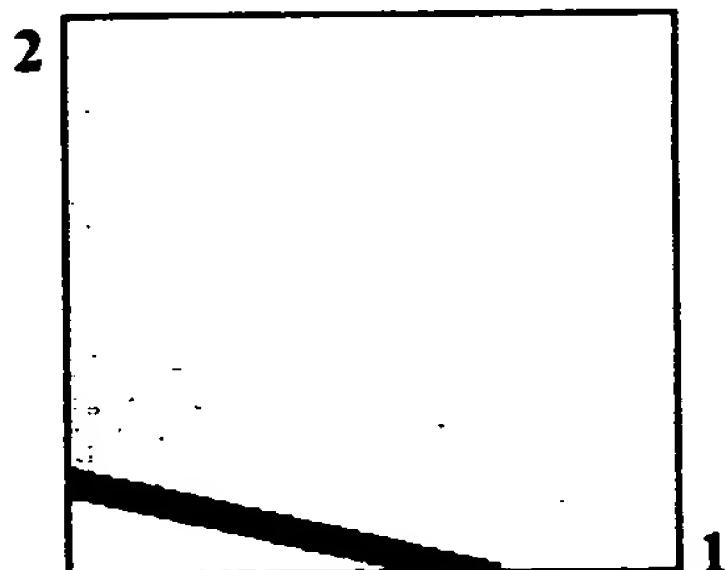
[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Nov-13-2000]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:   Filter  Align

Sequence 1 lcl|seq\_1 Length 137 (1 .. 137)

Sequence 2 lcl|seq\_2 Length 569 (1 .. 569)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 167 bits (87), Expect = 8e-40

Identities = 93/96 (96%)

Strand = Plus / Minus

Query: 1 ccggtaagtaaacagtcagaaaaattagcatgaaaggcagtttagcattggaggaagcaca 60

|||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct: 96 ccggtaagtaaacagtcagaaaaattagcatgaaaggcagtttagcattggaggaagctca 37

Query: 61 gatctctagagctgtccgtcgctgccaggattga 96

||||||||||||||||| ||||| ||||| ||||| |||||

Sbjct: 36 gatctctagagctgtccgtcgccgcaggattga 1

CPU time: 0.02 user secs. 0.04 sys. secs 0.06 total secs.

Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

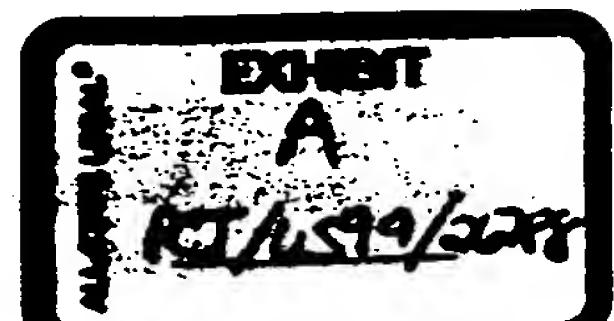
Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 1

Number of Sequences: 0

Number of extensions: 1

Number of successful extensions: 1



Number of sequences better than 10.0: 1  
length of query: 137  
length of database: 2,635,864,967  
effective HSP length: 22  
effective length of query: 115  
effective length of database: 2,635,864,945  
effective search space: 303124468675  
effective search space used: 303124468675  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 18 (35.3 bits)